- 28S

- 18S

Fig. 1A

- 28S

- 18S

Fig. 1B

```
   1        CTGGCTGCTGTGGAGTTTGTGACATACTAGGTGACACCCTTGGAGTCACTTC
  53 TCTTCAACTCCAGCTTAGAAGTGCCTGCCTGGCTCAGGGTCTGCACTGCAGCCTACTCCT
 113 TGCTTCAGGGCCTGACTGCAACGCCAAAGCCTATCCTATAGCGGCAGCGCCAGCAGCCAC
 173 TCAAACCAGCCACAGCTCCCCGGCAACCGAACCATGAACACCGAAATGTATCAGACCCCC
                                          MetAsnThrGluMetTyrGlnThrPro

 233 ATGGAGGTGGCGGTCTATCAGCTGCACAATTTCTCCACCTCCTTCTTTTCTTCTCTGCTT
     MetGluValAlaValTyrGlnLeuHisAsnPheSerThrSerPhePheSerSerLeuLeu

 293 GGAGGGGATGTGGTTTCCGTTAAACTGGATAACAGTGCCTCCGGAGCCAGTGTGGTGGCC
     GlyGlyAspValValSerValLysLeuAspAsnSerAlaSerGlyAlaSerValValAla

 353 CTAGACAACAAGATTGAGCAGGCCATGGACCTCGTGAAGAACCACCTGATGTACGCTGTG
     LeuAspAsnLysIleGluGlnAlaMetAspLeuValLysAsnHisLeuMetTyrAlaVal

 413 AGAGAGGAGGTGGAGGTCCTAAAGGAGCAGATTCGTGAGCTGCTTGAGAAGAACTCCCAG
     ArgGluGluValGluValLeuLysGluGlnIleArgGluLeuLeuGluLysAsnSerGln

 473 CTGGAGCGCGAGAACACCCTCCTGAAGACGCTGGCAAGCCCCGAGCAACTGGAAAAGTTC
     LeuGluArgGluLeuThrLeuLeuLysThrLeuAlaSerProGluGlnLeuGluLysPhe

 533 CAGTCCCGGCTGAGCCCTGAAGAGCCAGCACCTGAAGCCCCAGAAACCCCGGAAACCCCG
     GlnSerArgLeuSerProGluGluProAlaProGluAlaProGluThrProGluThrPro

 593 GAAGCCCCTGGTGGTTCTGCGGTGTAAGTGGCTCTGTCCTTAGGGTGGGCAGAGCCACAT
     GluAlaProGlyGlySerAlaVal *

 653 CTTGTTCTACCTAGTTCTTTCCAGTTTGTTTTTGGCTCCCCAAGGGTCATCTCATGTGGA
 713 GAACTTTACACCTAACATAGCTGGTGCCAAGAGATGTCCCAAGGACATGCCCATCTGGGT
 773 CCACTCCAGTGACAGACCCCTGACAAAGAGCAGGTCTCTGGAGACTAAGTTGCATGGGGC
 833 CTAGTAACACCAAGCCAGTGAGCCTGTCGTGTCACCGGGCCCTGGGGGCTCCCAGGGCTG
 893 GGCAACTTAGTTACAGCTGACCAAGGAGAAAGTAGTTTTGAGATGTGATGCCAGTGTGCT
 953 CCAGAAAGTGTAAGGGGTCTGTTTTTCATTTCCATGGACATCTTCCACAGCTTCACCTGA
1013 CAATGACTGTTCCTATGAAGAAGCCACTTGTGTTCTAAGCAGAAGCAACCTCTCTCTTCT
1073 TCCTCTGTCTTTTCCAGGCAGGGGCAGAGATGGGAGAGATTGAGCCAAATGAGCCTTCTG
1113 TTGGTTAATACTGTATAATGCATGGCTTTGTGCACAGCCCAGTGTGGGGTTACAGCTTTG
1193 GGATGACTGCTTATAAAGTTCTGTTTGGTTAGTATTGGCATCGTTTTTCTATATAGCCAT
1253 AATGCGTATATATACCCATAGGGCTAGATCTATATCTTAGGGTAGTGATGTATACATATA
1313 CACATACACCTACATGTTGAAGGGCCTAACCAGCTTTGGGAGTACTGACTGGTCTCTTAT
1373 CTCTTAAAGCTAAGTTTTTGACTGTGCTAATTTACCAAATTGATCCAGTTTGTCCTTTAG
1433 ATTAAATAAGACTCGATATGAGGGAGGGAGGGAAGACCAGCCTCACAATGCGGCCACAG
1493 ATGCCTTGCTGCTGCAGTCCTCCCTGATCTGTCCACTGAAGACATGAAGTCCTCTTTTGA
1553 ATGCCAAACCCACCATTCATTGGTGCTGACTACATAGAATGGGGTTGAGAGAAGATCAGT
1613 TTGGACTTCACATTTTTGTTTTAAGTTTTAGGTTGTTTTTTTTGGTTTTGTTTGTTTGT
1673 TTGTTTGTTTGTTTTTGTTTTTTGTTTTTCTTTTTTAAGTTCTTGTGGGGAAACTTTGGG
1733 GTTAATCAAAGGATGTAGTCCTGTGGTAGACCAGAGGAGTAACTAGTTTTGATCCTTTGG
1793 GGTGTGGAAAATGTACCCAGGAAGCTTGTGTAAGGAGGTTCTGTGACAGTGAACACTTTC
1853 CACTTTCTGACACCTCATCCTGCTGTACGACTCCAGGATTTGGATTTGGATTTTTCAAAT
1913 GTAGCTTGAAATTTCAATAAACTTTGCTCCTTTTTCTAAAAATAAAAAAAAAAAAAAAAA
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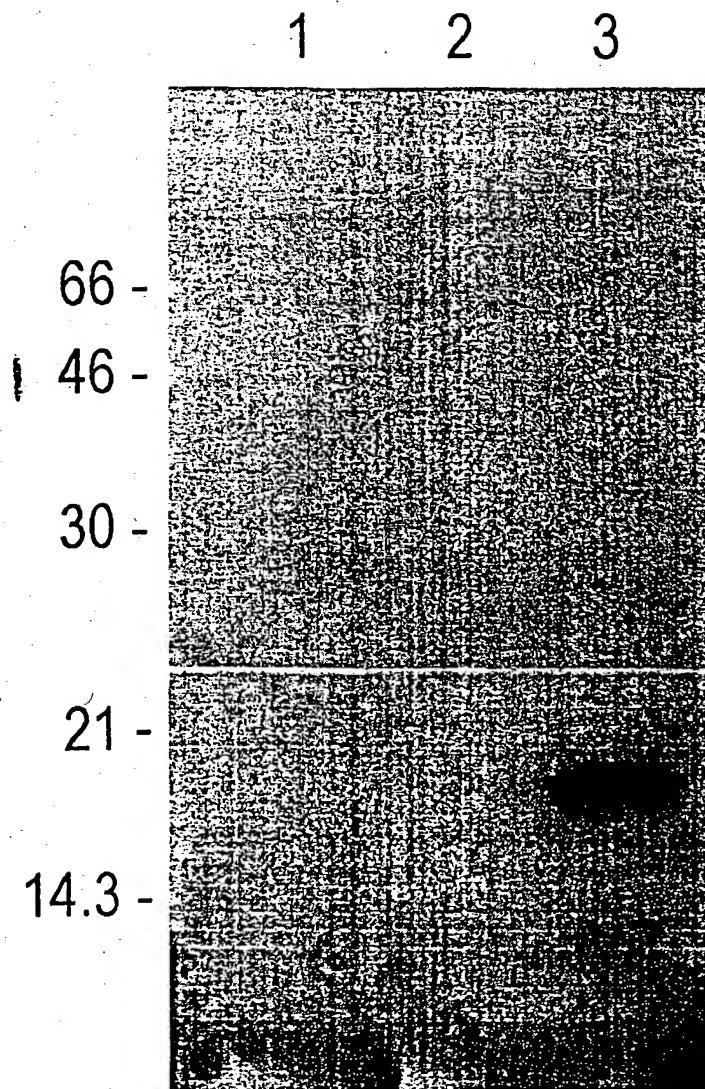
Fig. 2

Fig. 3A

Fig. 3B

Fig. 3C

GILR	L	K E Q I R E	L	L E K N S Q	L	E R E N T L	L	K T L A
TSC-22	L	K E Q I K E	L	I E K N S Q	L	E Q E N D L	L	K T L A
GCN4	L	E D K V E E	L	L S K N Y H	L	E N E V A R	L	K K L V
CREB	L	E N R V A V	L	E N Q N K T	L	I E E L K A	L	K D L Y
CREM	L	E N R V A V	L	E N Q N K T	L	I E E L K A	L	K D L Y
c-jun	L	E E K V K T	L	K A Q N S E	L	A S T A N M	L	R E Q V

Fig. 4

A

1 2 3 4 5 6 7 8 9   10

- 368 bp
- 244 bp

4 7 1 2 3 5 6 7 RNAi
pcDNA3   GILR

B

8   1 2 3 4 5 6 7

- 368 bp

- 244 bp

1 2 3 4 8 9 RNAi
pcDNA3   GILR

C

Eco-RI   ApaI

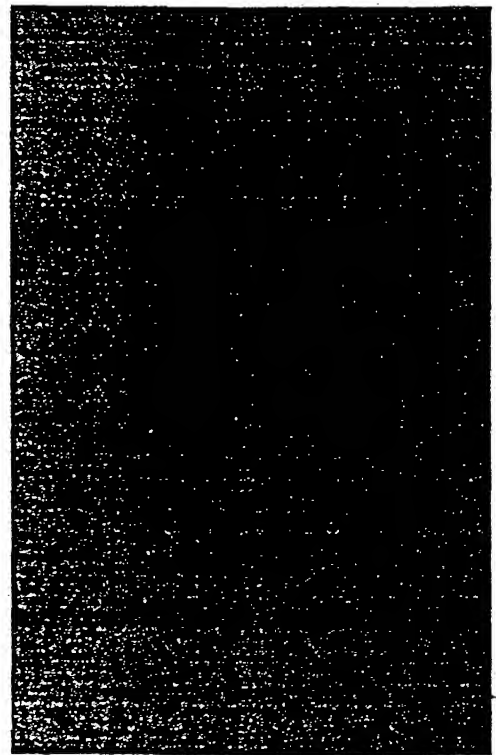pcDNA3   GILR cDNA   pcDNA3

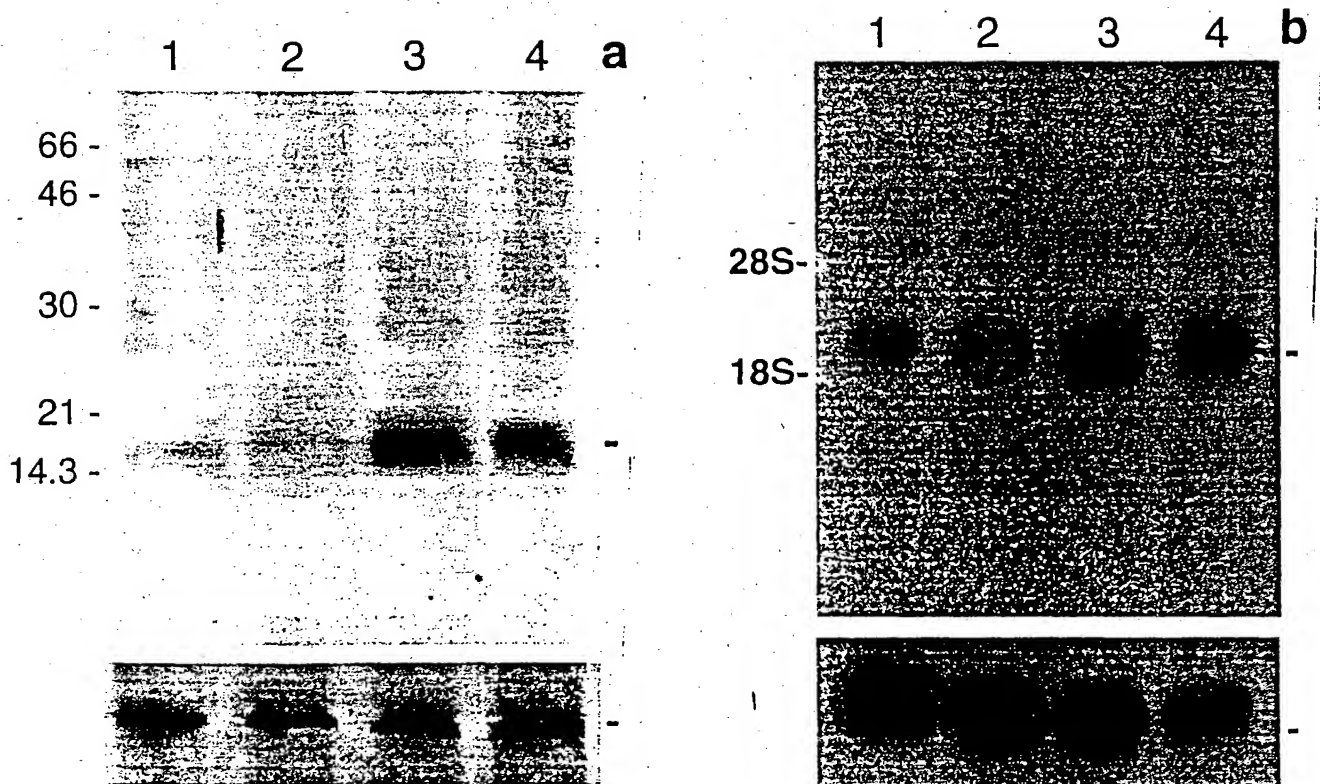Fig. 5

Fig. 6

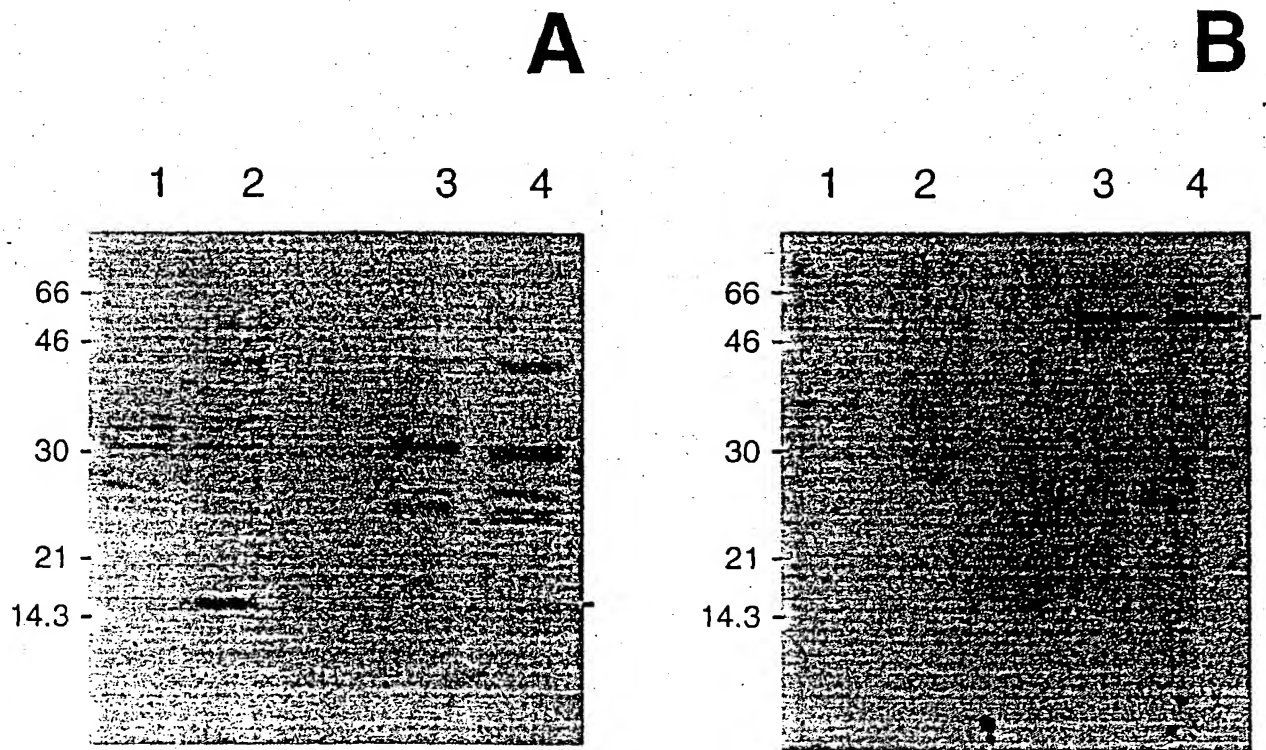Fig. 7

Fig.

Fig. 9

A

Fig. 10

B
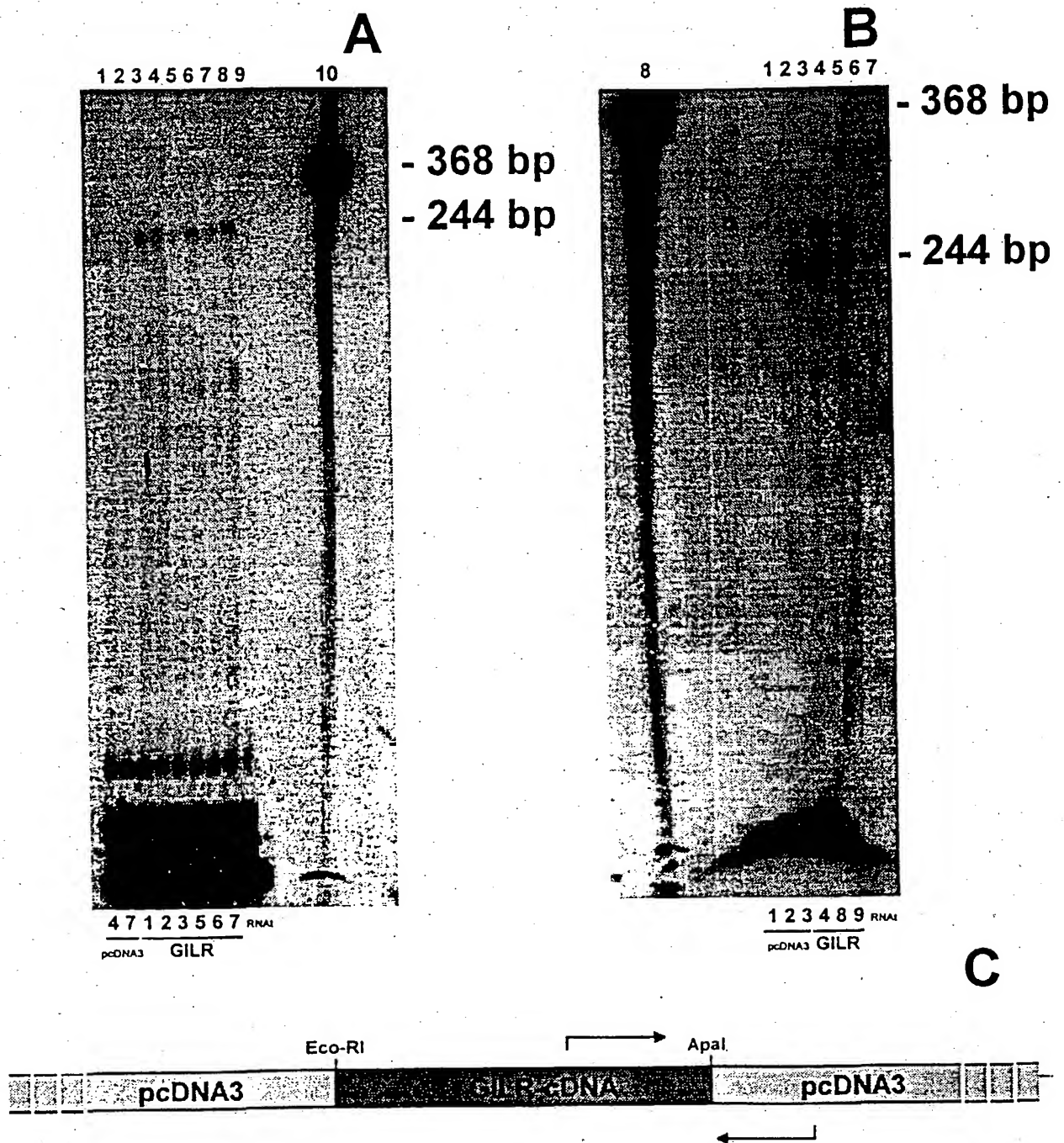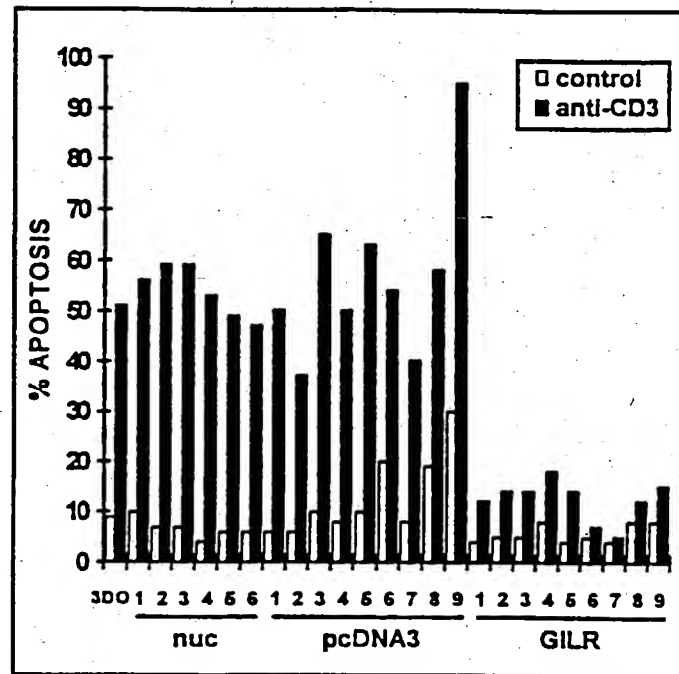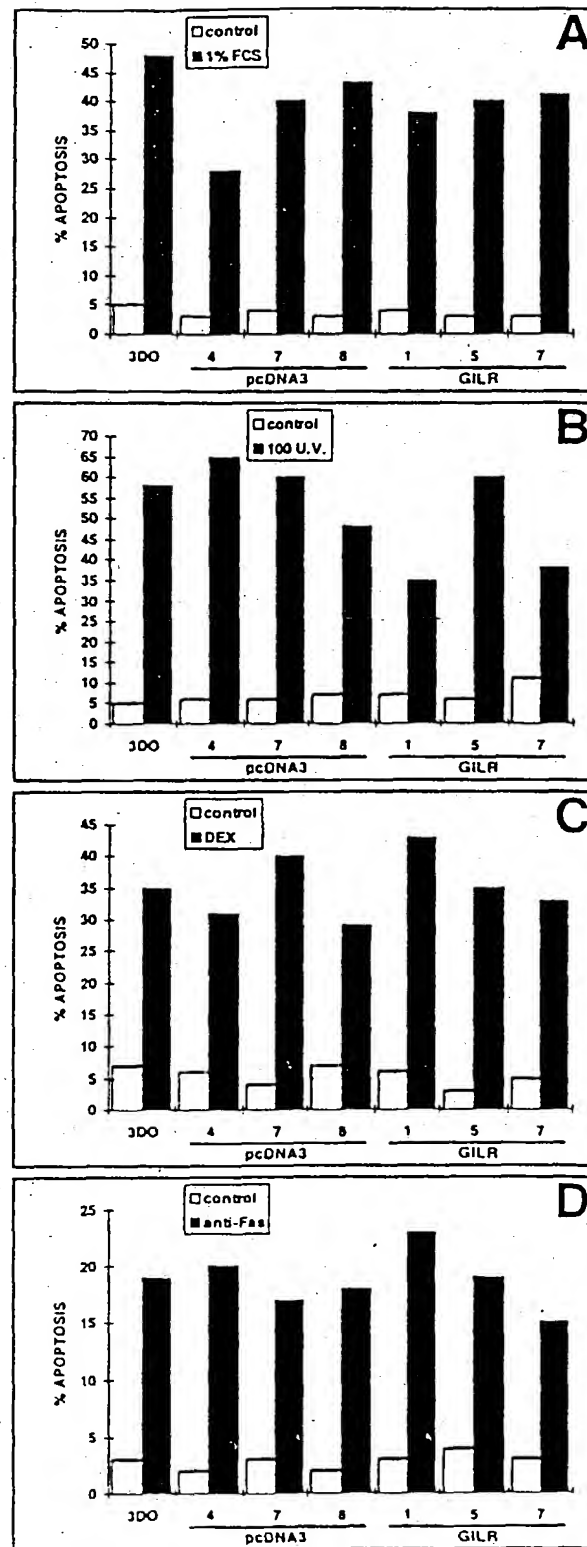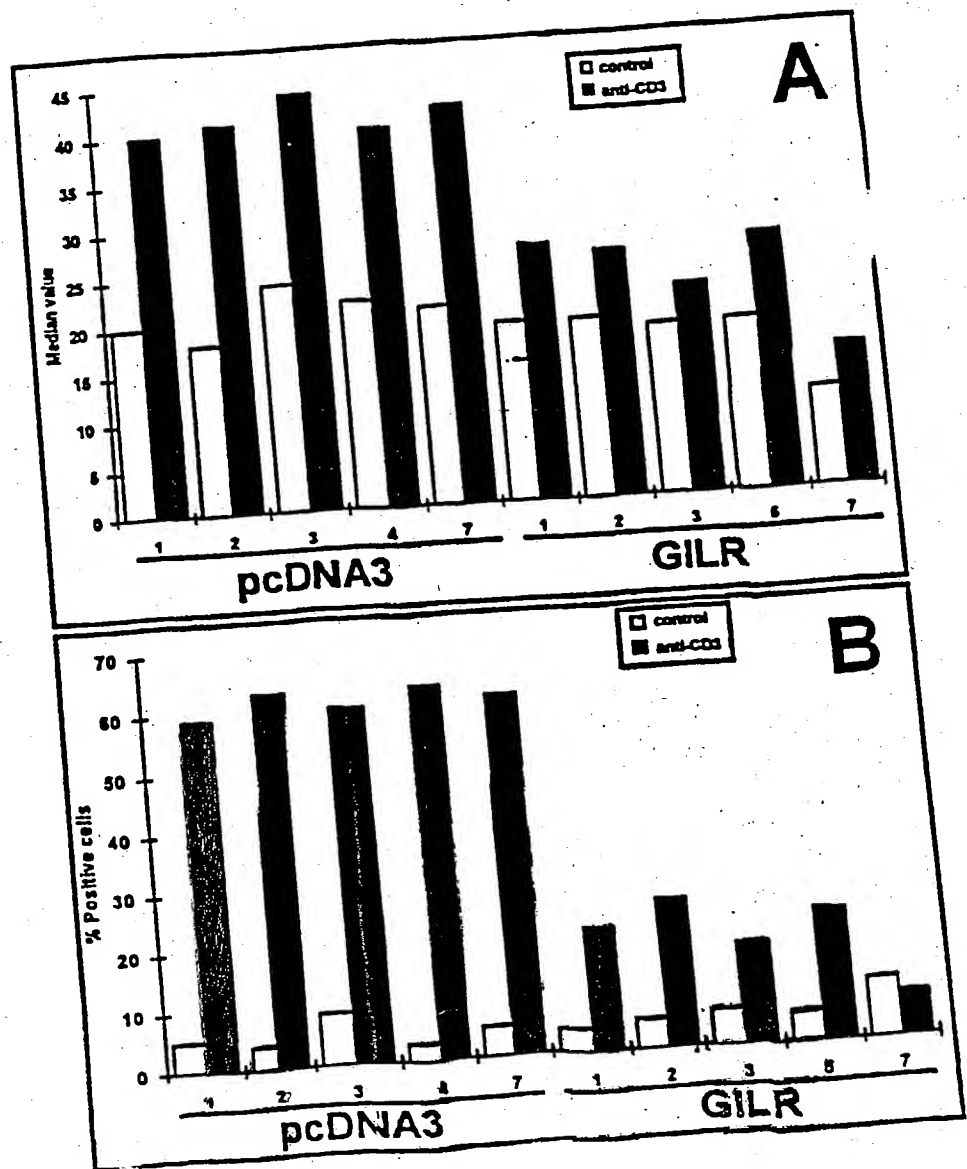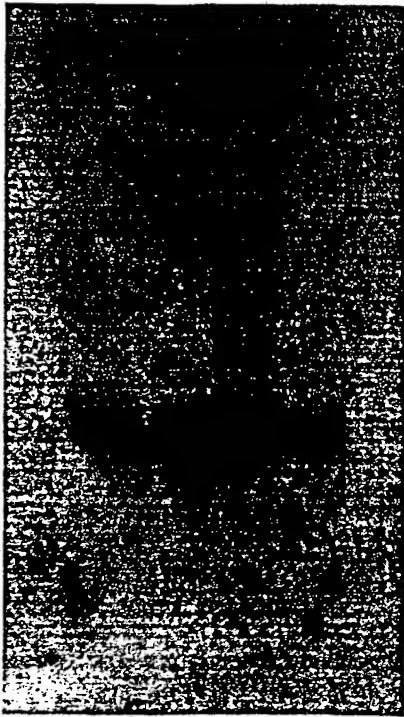
Fig. 11

Fig. 12

```
   1 AATTCGGGGGCCGTGGAGTTTGTGACATACGAGGTGACACCCCTCGAGTCACTTCCCTTC
  61 AACTCCAGCTGGAGCGCCTGCTTGGCTTTGGGTTCGTTCTGCAGCCTTCGCCCCGCTCCT
 121 AGCCTCAGGGCCGGACTCCAGCGCAGAGCCCAGCCCAGCGCAGCCTGCCAGCAGCCACCC
 181 AGCCGCCCAGCCGCCCAGCCCCGCACGAAACCCGGCCAGAGCTTCCTAGCAGCCCGAGCC
 241 ATGAACACCGAAATGTATCAGACCCCCATGGAGGTGGCGGTCTACCAGCTGCACAATTTC
     MetAsnThrGluMetTyrGlnThrProMetGluValAlaValTyrGlnLeuHisAsnPhe

 301 TCCATCTCCTTCTTCTCTTCTGCTTGGAGGGGATGTGGTTTCCGTTAAGCTGGACAAC
     SerIleSerPhePheSerSerLeuLeuGlyGlyAspValValSerValLysLeuAspAsn

 361 AGTGCCTCCGGAGCCAGCGTGGTGGCCATAGACAACAAGATCGAACAGGCCATGGATCTG
     SerAlaSerGlyAlaSerValValAlaIleAspAsnLysIleAspGlnAlaMetAspLeu

 421 GTGAAGAATCATCTGATGTATGCTGTGAGAGAGGAGGTGGAGATCCTGAAGGAGCAGATC
     ValLysAsnHisLeuMetTyrAlaValArgGluGluValGluIleLeuLysGluGlnIle

 481 CGAGAGCTGGTGGAGAAGAACTCCCAGCTAGAGCGTGAGAACACCCTGTTGAAGACCCTG
     ArgGluLeuValGluLysAsnSerGlnLeuGluArgGluAsnThrLeuLeuLysThrLeu

 541 GCAACCCCAGAGCAGCTGGAGAAGTTCCAGTCCTGTCTGAGCCCTGAAGAGCCAGCTCCC
     AlaSerProGluGlnLeuGluLysPheGlnSerCysLeuSerProGluGluProAlaPro

 601 GAATCCCCACAAGTGCCCGAGGCCCCTGGTGGTTCTGCGGTGTAAGTGGCTCTGTCCTCA
     GluSerProGlnValProGluAlaProGlyGlySerAlaVal *

 661 GGGTGGGCAGAGCCACTAAACTTGTTTTACCTAGTTCTTTCCAGTTTGTTTTTGGCTCCC
 721 CAAGCATCATCTCACGAGGAGAACTTTACACCTAGCACAGCTGGTGCCAAGAGATGTCCT
 781 AAGGACATGGCCACCTGGGTCCACTCCAGCGACAGACCCCTGACAAGAGCAGGTCTCTGG
 841 AGGCTGAGTTGCATGGGGCCTAGTAACACCAAGCCAGTGAGCCTCTAATGCTACTGCGCC
 901 CTGGGGGCTCCCAGGGCCTGGGCAACTTAGCTGCAACTGGCAAAGGAGAAGGGTAGTTTG
 961 AGGTGTGACACCAGTTTGCTCCAGAAAGTTTAAGGGGTCTGTTTCTCATCTCCATGGACA
1021 TCTTCAACAGCTTCACCTGACAACGACTGTTCCTATGAAGAAGCCACTTGTGTTTTAAGC
1081 AGAGGCAACCTCTCTCTTCTCCTCTGTTTCGTGAAGGCAGGGGACACAGATGGGAGAGAT
1141 TGAGCCAAGTCAGCCTTCTGTTGGTTAATATGGTATAATGCATGGCTTTGTGCACAGCCC
1201 AGTGTGGGATTACAGCTTTGGGATGACCGCTTACAAAGTTCTGTTTGGTTAGTATTGGCA
1261 TAGTTTTTCTATATAGCCATAAATGCGTATATATACCCATAGGGCTAGATCTGTATCTTA
1321 GTGTAGCGATGTATACATATACACATCCACCTACATGTTGAAGGGCCTAACCAGCCTTGG
1381 GAGTATTGACTGGTCCCTTACCTCTTATGGCTAAGTCTTTGACTGTGTTCATTTACCAAG
1441 TTGACCCAGTTTGTCTTTTAGGTTAAGTAAGAACTCGAGAGTAAAGGCAAGGAGGGGGGC
1501 CAGCCTCTGAATGCGGCCACGGATGCCTTGCTGCTGCAACCCTTTCCCCAGCTGTCCACT
1561 GAAACGTGAAGTCCTGTTTTGAATGCCAAACCCACCATTCACTGGTGCTGACTACATAGA
1621 ATGGGTTGAGAGAAGATCAGTTTGGGCTTCACAGTGTCATTTGAAAAAGCGTTTTTGTTT
1681 TGTTTTGAATTATTGTGGAAAACTTTCAAGTGAACAGAAGGATGGTGTCCTACTGTGGAT
1741 GAGGGATGAACAAGGGGATGGCTTTGATCCAATGGAGCCTGGGAGGTGTGCCCAGAAAGC
1801 TTGTCTGTAGCGGGTTTTGTGAGAGTGAACACTTTCCACTTTTTGACACCTTATCCTGAT
1861 GTATGGTTCCAGGATTTGGATTTTGATTTTCCAAATGTAGCTTGAAATTTCAATAAACTT
1921 TGCTCTGTTTTTCTAAAAAATAAAAA
```

Fig. 13

```
  1 ...CTGGCTGCTGTGGAGTTTGTGACATACTAGGTGACACCCTTGGAGTC 47
        ||   ||  |||||||||||||||||||| |||||||||| | |||||
  1 aattcggggggccgtggagtttgtgacatacgaggtgacacccctcgagtc 50

 48 ACTTCTCTTCAACTCCAGCTTAGAAGTGCCTGCCTGGCTCAGGGTCTGCA 97
    |||||  |||||||||||||||| | || ||||||| ||||||  |||| |
 51 acttcccttcaactccagct..ggagcgcctgcttggctttgggttcgtt 98

 98 CTGCAGCCT.......ACTCCTTGCTTCAGGGCCTGACTGCAACGCCAAA 140
    |||||||||         ||||| || ||||||||| |||| || ||| |
 99 ctgcagccttcgccccgctcctagcctcagggccggactccagcgcagag 148

141 GCCTATCC......................TATAGCGGCAGCGCCA 164
     ||    ||                         | || || |
149 cccagcccagcgcagcctgccagcagccacccagccgcccagccgcccag 198

165 GCAGCCACTCAAACCAGCCACAGCTCCCCGGCA.ACCGAACCATGAACAC 213
     |    |||   || || |||| |||| ||  ||| |||| |||||||||||
199 ccccgcacgaaacccggccagagcttcctagcagcccgagccatgaacac 248

214 CGAAATGTATCAGACCCCCATGGAGGTGGCGGTCTATCAGCTGCACAATT 263
    |||||||||||||||||||||||||||||||||||||||| |||||||||||
249 cgaaatgtatcagacccccatggaggtggcggtctaccagctgcacaatt 298

264 TCTCCACCTCCTTCTTTTCTTCTCTGCTTGGAGGGGATGTGGTTTCCGTT 313
    ||||||  |||||||||  ||||||||||||||||||||||||||||||||
299 tctccatctccttcttctcttctctgcttggaggggatgtggtttccgtt 348

314 AAACTGGATAACAGTGCCTCCGGAGCCAGTGTGGTGGCCCTAGACAACAA 363
    || |||||  |||||||||||||||||||||||||| ||||||||| |||||||||||
349 aagctggacaacagtgcctccggagccagcgtggtggccatagacaacaa 398

364 GATTGAGCAGGCCATGGACCTCGTGAAGAACCACCTGATGTACGCTGTGA 413
    ||| || |||||||||| || ||||||||| || |||||||||.|||||||
399 gatcgaacaggccatggatctggtgaagaatcatctgatgtatgctgtga 448

414 GAGAGGAGGTGGAGGTCCTAAAGGAGCAGATTCGTGAGCTGCTTGAGAAG 463
    ||||||||||||||| |||| |||||||||| || |||||| | ||||||
449 gagaggaggtggagatcctgaaggagcagatccgagagctggtggagaag 498

464 AACTCCCAGCTGGAGCGCGAGAACACCCTCCTGAAGACGCTGGCAAGCCC 513
    |||||||||| |||||| ||||||||||||   ||||||| |||||||||||
499 aactcccagctagagcgtgagaacaccctgttgaagaccctggcaagccc 548

514 CGAGCAACTGGAAAAGTTCCAGTCCCGGCTGAGCCCTGAAGAGCCAGCAC 563
    ||||| ||||| ||||||||||||||||| |||||||||||||||||||| |
549 agagcagctggagaagttccagtcctgtctgagccctgaagagccagctc 598

564 CTGAAGCCCCAGAAACCCCGGAAACCCCGGAAGCCCCTGGTGGTTCTGCG 613
    | ||| |||||         ||   || || |||||||||||||||||||||
599 ccgaatcccca.........caagtgcccgaggcccctggtggttctgcg 639
```

Fig. 14

```
 614 GTGTAAGTGGCTCTGTCCTTAGGGTGGGCAGAGCCAC..ATCTTGTTCTA 661
     |||||||||||||||||| ||||||||||||||||| | |||||| ||
 640 gtgtaagtggctctgtcctcagggtgggcagagccactaaacttgtttta 689

 662 CCTAGTTCTTTCCAGTTTGTTTTTGGCTCCCCAAGGGTCATCTCATGTGG 711
     ||||||||||||||||||||||||||||||||| |||||||| | ||
 690 cctagttctttccagtttgtttttggctccccaagcatcatctcacgagg 739

 712 AGAACTTTACACCTAACATAGCTGGTGCCAAGAGATGTCCCAAGGACATG 761
     |||||||||||||| || ||||||||||||||||||||| |||||||||
 740 agaactttacacctagcacagctggtgccaagagatgtcctaaggacatg 789

 762 CCCATCTGGGTCCACTCCAGTGACAGACCCCTGACAAAGAGCAGGTCTCT 811
     ||| |||||||||||||||||| |||||||||| |||||||||||||||
 790 gccacctgggtccactccagcgacagacccctgac.aagagcaggtctct 838

 812 GGAGACTAAGTTGCATGGGGCCTAGTAACACCAAGCCAGTGAGCCTGTCG 861
     |||| || |||||||||||||||||||||||||||||||||||||||| |
 839 ggaggctgagttgcatggggcctagtaacaccaagccagtgagcctctaa 888

 862 TGTCACCGGGCCCTGGGGGCTCCCAGGG.CTGGGCAACTTAGTTACAGCT 910
     ||   || | |||||||||||||||||| ||||||||||| | || ||
 889 tgctactgcgccctggggggctcccagggcctgggcaacttagctgcaact 938

 911 GACCAAGGAGAAAGTAGTTTTGAGATGTGATGCCAGTGTGCTCCAGAAAG 960
     | | |||||||| | ||||||| ||||| |||||| ||||||||||||
 939 ggcaaggagaagggtagtttgaggtgtgacaccagtttgctccagaaag 988

 961 TGTAAGGGGTCTGTTTTTCATTTCCATGGACATCTTCCACAGCTTCACCT 1010
     | ||||||||||||||| |||| |||||||||||||| ||||||||||||
 989 tttaaggggtctgtttctcatctccatggacatcttcaacagcttcacct 1038

1011 GACAATGACTGTTCCTATGAAGAAGCCACTTGTGTTCTAAGCAGAAGCAA 1060
     |||||| ||||||||||||||||||||||||||||||||| |||||||| ||||
1039 gacaacgactgttcctatgaagaagccacttgtgttttaagcagaggcaa 1088

1061 CCTCTCTCTTCTTCCTCTGTCTTTTCCAGGCAGGGG.CAGAGATGGGAGA 1109
     |||||||||| |||||||| | |   ||||||||| || |||||||||||
1089 cctctctcttc.tcctctgtttcgtgaaggcaggggacacagatgggaga 1137

1110 GATTGAGCCAAATGAGCCTTCTGTTGGTTAATACTGTATAATGCATGGCT 1159
     ||||||||||| | ||||||||||||||||||| |||||||||||||||
1138 gattgagccaagtcagccttctgttggttaatatggtataatgcatggct 1187

1160 TTGTGCACAGCCCAGTGTGGGGTTACAGCTTTGGGATGACTGCTTATAAA 1209
     |||||||||||||||||||||||| ||||||||||||||||| ||||| |||
1188 ttgtgcacagcccagtgtgggattacagctttgggatgaccgcttacaaa 1237

1210 GTTCTGTTTGGTTAGTATTGGCATCGTTTTTCTATATAGCCAT.AATGCG 1258
     |||||||||||||||||||||||| ||||||||||||||||||| ||||||
1238 gttctgtttggttagtattggcatagtttttctatatagccataaatgcg 1287

1259 TATATATACCCATAGGGCTAGATCTATATCTTAGGGTAGTGATGTATACA 1308
     |||||||||||||||||||||||| ||||||||| |||| ||||||||||
1288 tatatatacccatagggctagatctgtatcttagtgtagcgatgtataca 1337
```

Fig. 14 (cont)

```
1309 TATACACATACACCTACATGTTGAAGGGCCTAACCAGCTTTGGGAGTACT 1358
     |||||||||| ||||||||||||||||||||||||||||| ||||||||| |
1338 tatacacatccacctacatgttgaagggcctaaccagccttgggagtatt 1387

1359 GACTGGTCTCTTATCTCTTAAAGCTAAGTTTTTGACTGTGCTAATTTACC 1408
     |||||||| |||| |||||| ||||||| |||||||||| | |||||||
1388 gactggtcccttacctcttatggctaagtctttgactgtgttcatttacc 1437

1409 AAATTGATCCAGTTTGTCCTTTAGATTAAATAAG.ACTCGATATGAGGGA 1457
     || |||| |||||||||| ||||| |||| |||| |||||| |  |  |
1438 aagttgacccagtttgtctttaggttaagtaagaactcgagagtaaagg 1487

1458 GGGAGGGGAAGACCAGCCTCACAATGCGGCCACAGATGCCTTGCTGCTGC 1507
      | || | |||||||| ||||||||| |||||||||||||||||||||
1488 caaggagggggggccagcctctgaatgcggccacggatgccttgctgctgc 1537

1508 AGTCC.TCCCTGATCTGTCCACTGAAGACATGAAGTCCTCTTTTGAATGC 1556
     | || | || | |||||||||||| || ||||||||| |||||||||
1538 aaccctttccccagctgtccactgaa.acgtgaagtcctgttttgaatgc 1586

1557 CAAACCCACCATTCATTGGTGCTGACTACATAGAATGGGGTTGAGAGAAG 1606
     ||||||||||||||| ||||||||||||||||||||||| |||||||||||
1587 caaacccaccattcactggtgctgactacatagaat.gggttgagagaag 1635

1607 ATCAGTTTGGACTTCACATTTTTGTTTTAAGTTTTAGGTTGTTTTTTTTT 1656
     |||||||||| ||||||| | | ||| ||  |  ||||||| |||
1636 atcagtttgggcttcacagtgtcatttgaa.....aaagcgttttgttt 1680

1657 GGTTTTGTTTGTTTGTTTGTTTGTTTGTTTTTGTTTTTTGTTTTTCTTTT 1706
     |||||| | ||||
1681 tgttttgaattattgt.............................. 1696

1707 TTAAGTTCTTGTGGGGAAACTTTGGGGTTAATCAAAGGATGTAGTCCTGT 1756
              || ||||||| || ||  ||||||| ·|||||
1697 ...........ggaaactttcaagtgaacagaaggatggtgtcctac 1733

1757 GGTAGACCAG......AGGAGTAACTAGTTTTGATCCTTTGGGGTGTGGA 1800
     || || ||   · | || | | ||||||| ||| | |||
1734 tgtggatgagggatgaacaaggggatggctttgatccaatggagcctggg 1783

1801 AAATGTACCCAGGAAGCTTGTGT.AAGGAGGTTCTGTGACAGTGAACACT 1849
     ·| ||| |||||| ||||||||· | || |||| ||||| |||||||||||
1784 aggtgtgcccagaaagcttgtctgtagcgggttttgtgagagtgaacact 1833

1850 TTCCACTTTCTGACACCTCATCCTGCTGTACGACTCCAGGATTTGGATTT 1899
     |||||||||| |||||||| ||||||| |||| | |||||||||||||||
1834 ttccactttttgacaccttatcctgatgtatggttccaggatttggattt 1883

1900 GGATTTTTCAAATGTAGCTTGAAATTTCAATAAACTTTGCTCCTTTTTCT 1949
     ||||||| |||||||||||||||||||||||||||||||||||| ||||
1884 tgattttccaaatgtagcttgaaatttcaataaactttgctctgttttttc 1933

1950 AAAAATAAAAAAAAAAAAAAAAA 1972
     |||| | |||||
1934 taaaaaataaaaa......... 1946
```

Fig. 14 (Cont.)

```
mG    1  MNTEMYQTPMEVAVYQLHNFSTSFFSSLLGGDVVSVKLDNSASGASVVAL  50

hG    1  MNTEMYQTPMEVAVYQLHNFSISFFSSLLGGDVVSVKLDNSASGASVVAI  50
         =================== ==========================-

hT    2  KSQWCRPVAMDLGVYQLRHFSISFLSSLLGTENASVRLDNSSSGASVVAI  51
            =------=== == == ===== -  ==-===-========


mG   51  DNKIEQAMDLVKNHLMYAVREEVEVLKEQIRELLEKNSQLERENTLLKTL  100

hG   51  DNKIEQAMDLVKNHLMYAVREEVEILKEQIRELVEKNSQLERENTLLKTL  100
         ==========================-========-=============

hT   52  DNKIEQAMDLVKSHLMYAVREEVEVLKEQIKELIEKNSQLEQENNLLKTL  101
         ===========  ================-==-=======-== =====

hD    1          MDLVKNHLMYAVREEVEILKEQIRELVEKNSQLERENTLLKTL  41
                 ================-========-=======-=========


mG  101  ASPEQLEKFQSRLSPEEPAPEAPETPETPEAPGGSAV*  138

hG  101  ASPEQLEKFQSCLSPEEPAPES...PQVPEAPGGSAV*  135
         ===========  ==========-   =- =========

hT  102  ASPEQLAQFQAQLQTGSPPATTQPQGTTQPPAQPASQGSGPTA*  145
         ======  -==- =    =    -       =

hD   42  ASPEQLEKFQSCLSPEEPAPES...PQVPEAPGGSAV*
         =======-=== =========-   ============
```

Fig. 15

Mouse GILR

5' hCD2 promoter   Intron   Poly A signal   hCD2 LCR   3'

FIG. 16A

GO-TG WT WT GO-TG WT GO-TG GO-TG GO-TG WT

Human CD2 -
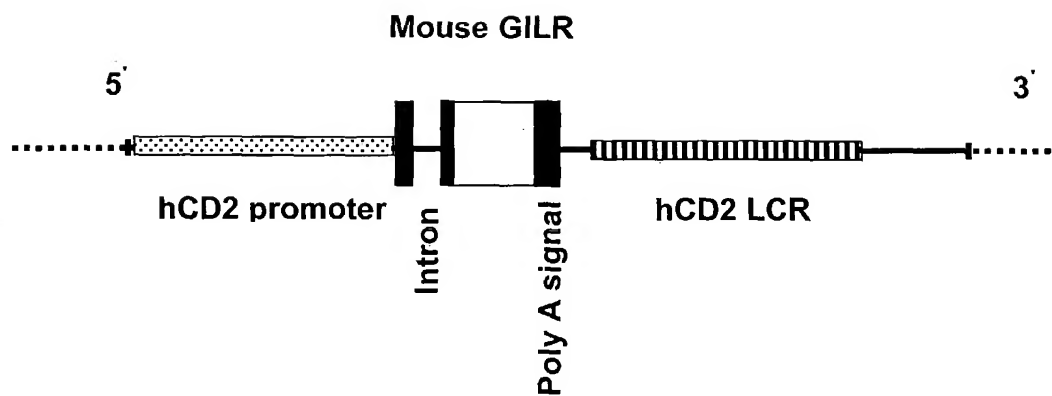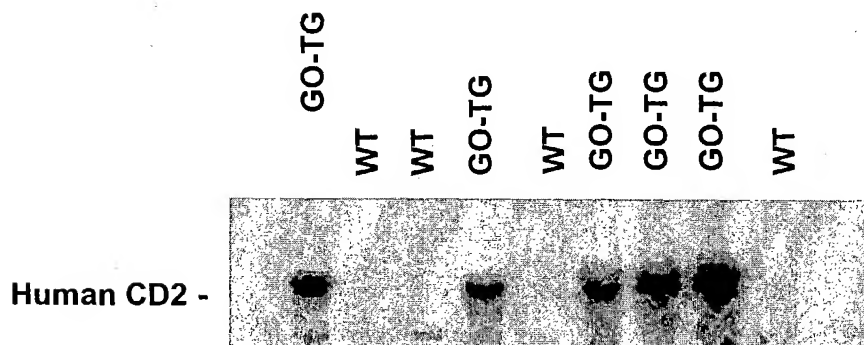
FIG. 16B

FIG. 17A

FIG. 17B

FIG. 18A

WT

11.7±0.	79.4±0.
4.6±0.	4.3±0.4

CD4 (+/−), CD8 (−/+)

GO-TG

13.7±1	74±1.8*
6±0.3*	6.2±0.8*

CD4 (+/−), CD8 (−/+)

FIG. 18B

WT

GO-TG

12.4

12.4%

M1

21.5

21.5%

M1
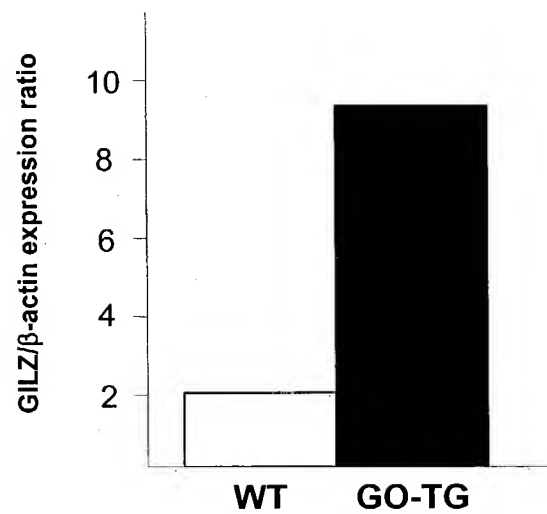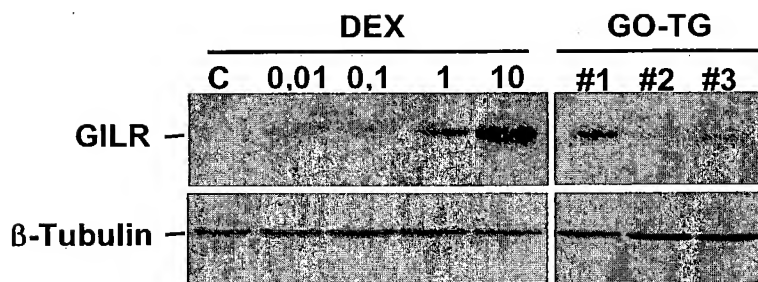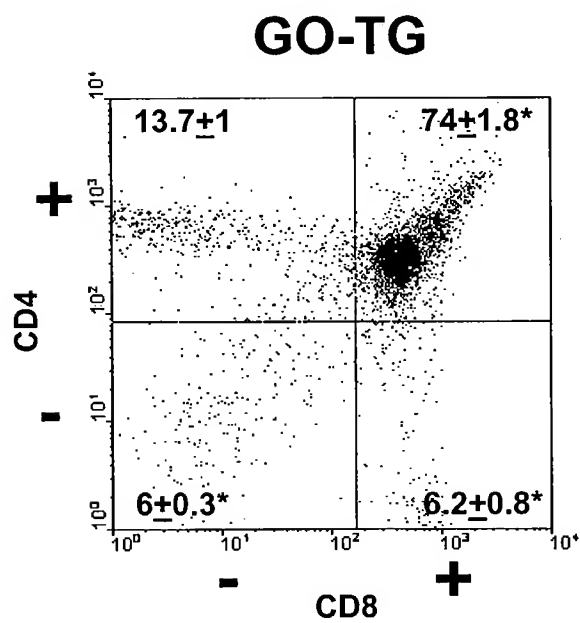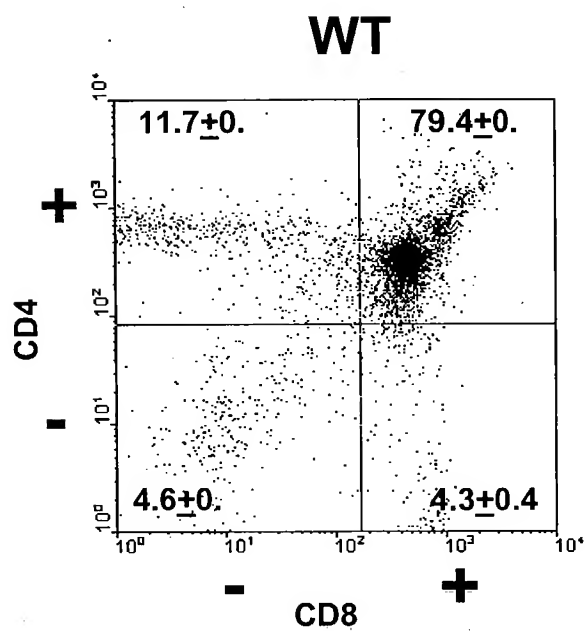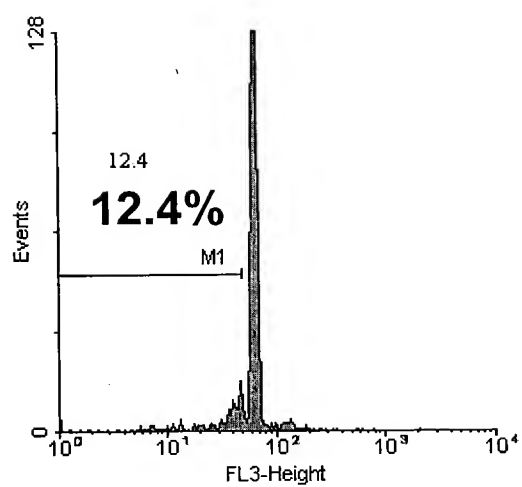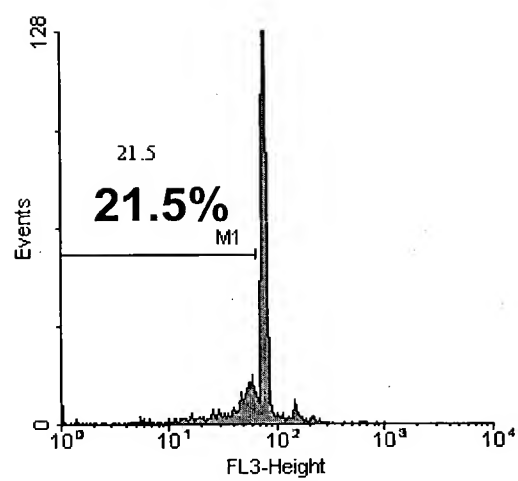
FIG. 19A

FIG. 19B
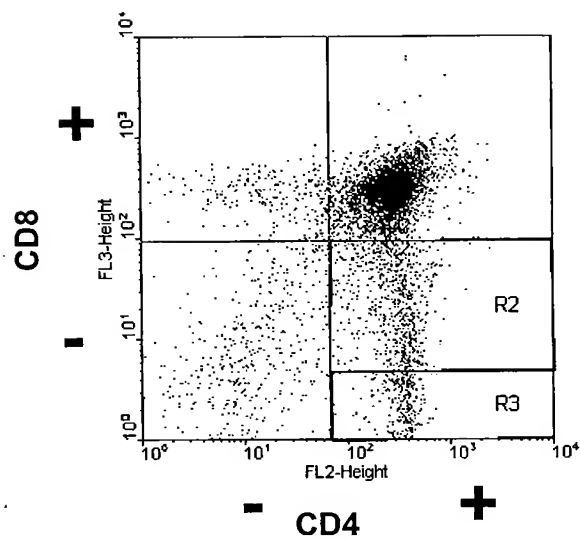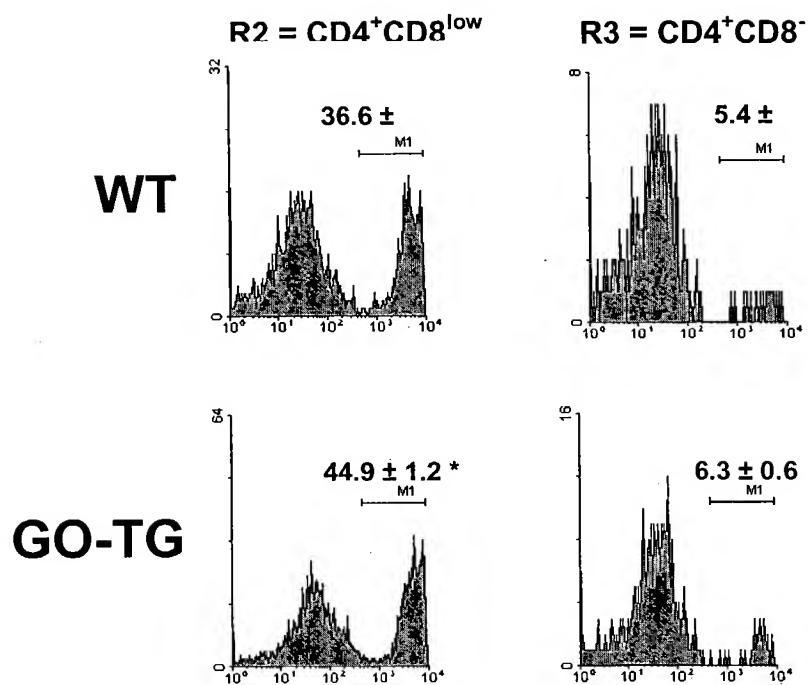
FIG. 20A

FIG. 20B

FIG. 21A
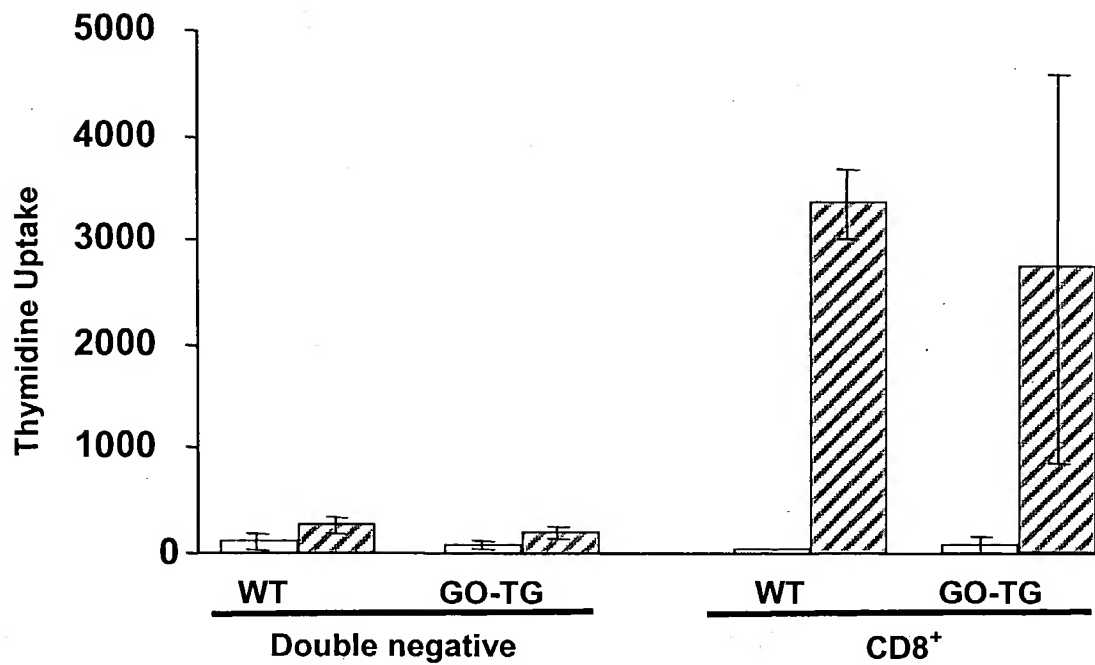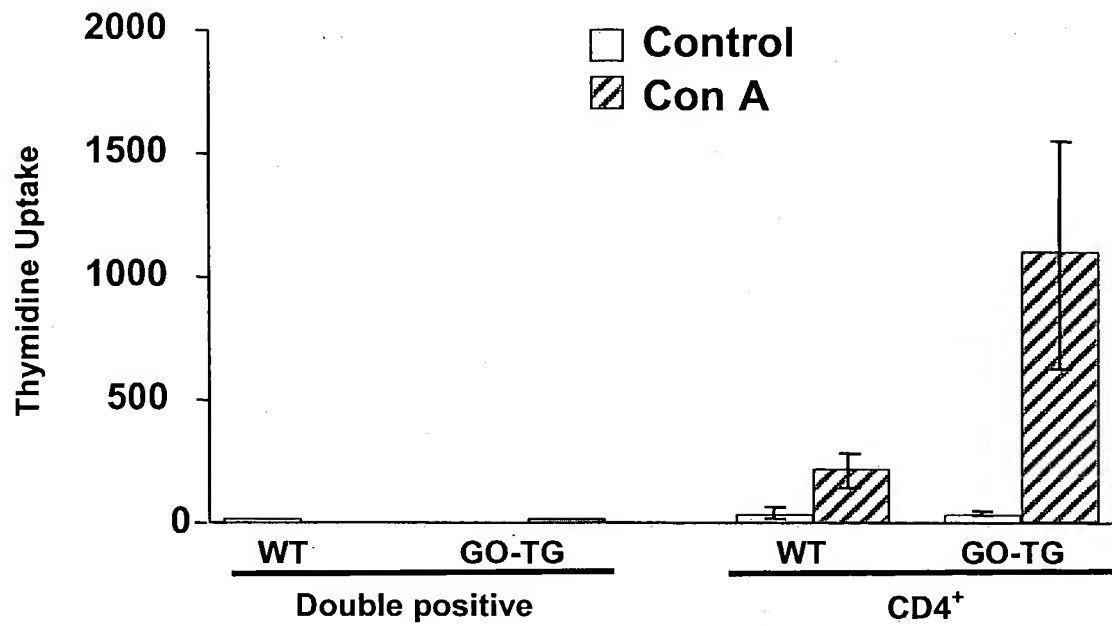
FIG. 21B

FIG. 22

FIG. 23

FIG. 24